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RAW SEQUENCE LISTING                          DATE: 02/26/2002
PATENT APPLICATION:  US/09/856,371A           TIME: 09:28:41

          Input Set : A:\sequence listing.txt
          Output Set: N:\CRF3\02262002\I856371A.raw

    3 <110> APPLICANT: UEMURA, Hidetoshi
    4         OKUI, Akira
    5         KOMINAMI, Katsuya
    6         YAMAGUCHI, Nozomi
    7         MITSUI, Shinichi
    9 <120> TITLE OF INVENTION: NOVEL SERINE PROTEASE BSSP2
   11 <130> FILE REFERENCE: UEMURA=7
   13 <140> CURRENT APPLICATION NUMBER: 09/856,371A
C--> 14 <141> CURRENT FILING DATE: 1999-11-19
   16 <150> PRIOR APPLICATION NUMBER: JP 10/347785
   17 <151> PRIOR FILING DATE: 1998-11-20
   19 <150> PRIOR APPLICATION NUMBER: PCT/JP99/06475
   20 <151> PRIOR FILING DATE: 1999-11-19
   22 <160> NUMBER OF SEQ ID NOS: 44
   24 <170> SOFTWARE: PatentIn version 3.1
   26 <210> SEQ ID NO: 1
   27 <211> LENGTH: 717
   28 <212> TYPE: DNA
   29 <213> ORGANISM: Mus sp.
   31 <220> FEATURE:
   32 <221> NAME/KEY: CDS
   33 <222> LOCATION: (1)..(717)
   34 <223> OTHER INFORMATION:
   37 <400> SEQUENCE: 1
   38 ata gtt ggc ggc caa gct gtg gct tct ggg cgc tgg cca tgg caa gct      48
   39 Ile Val Gly Gly Gln Ala Val Ala Ser Gly Arg Trp Pro Trp Gln Ala
   40 1               5                   10                  15
   42 agc gtg atg ctt ggc tcc cgg cac acg tgt ggg gcc tct gtg ttg gca      96
   43 Ser Val Met Leu Gly Ser Arg His Thr Cys Gly Ala Ser Val Leu Ala
   44             20                  25                  30
   46 cca cac tgg gta gtg act gct gcc cac tgc atg tac agt ttc agg ctg     144
   47 Pro His Trp Val Val Thr Ala Ala His Cys Met Tyr Ser Phe Arg Leu
   48             35                  40                  45
   50 tcc cgc cta tcc agc tgg cgg gtt cat gca ggg ctg gtc agc cat ggt     192
   51 Ser Arg Leu Ser Ser Trp Arg Val His Ala Gly Leu Val Ser His Gly
   52         50                  55                  60
   54 gct gtc cga caa cac cag gga act atg gtg gag aag atc att cct cat     240
   55 Ala Val Arg Gln His Gln Gly Thr Met Val Glu Lys Ile Ile Pro His
   56 65                  70                  75                  80
   58 cct ttg tac agt gcc cag aac cat gac tat gat gtg gct ctg ctg cag     288
   59 Pro Leu Tyr Ser Ala Gln Asn His Asp Tyr Asp Val Ala Leu Leu Gln
   60                 85                  90                  95
   62 ctc cgg aca cca atc aac ttc tca gac acc gtg gac gct gtg tgc ttg     336
```

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63 Leu Arg Thr Pro Ile Asn Phe Ser Asp Thr Val Asp Ala Val Cys Leu
64           100             105             110
66 ccg gcc aag gag cag tac ttt cca tgg ggg tcg cag tgc tgg gtg tct      384
67 Pro Ala Lys Glu Gln Tyr Phe Pro Trp Gly Ser Gln Cys Trp Val Ser
68           115             120             125
70 ggc tgg ggc cac acc gac ccc agc cat act cat agc tca gat aca ctg      432
71 Gly Trp Gly His Thr Asp Pro Ser His Thr His Ser Ser Asp Thr Leu
72           130             135             140
74 cag gac aca atg gta ccc ctg ctc agc acc cac ctc tgc aac agc tca      480
75 Gln Asp Thr Met Val Pro Leu Leu Ser Thr His Leu Cys Asn Ser Ser
76 145             150             155             160
78 tgc atg tac agt ggg gca ctt aca cac cgc atg ttg tgt gct ggc tac      528
79 Cys Met Tyr Ser Gly Ala Leu Thr His Arg Met Leu Cys Ala Gly Tyr
80           165             170             175
82 ctg gat gga agg gca gac gca tgc cag gga gac agc ggg gga ccc ctg      576
83 Leu Asp Gly Arg Ala Asp Ala Cys Gln Gly Asp Ser Gly Gly Pro Leu
84           180             185             190
86 gta tgt ccc agt ggt gac acg tgg cac ctt gta ggg gtg gtc agc tgg      624
87 Val Cys Pro Ser Gly Asp Thr Trp His Leu Val Gly Val Val Ser Trp
88           195             200             205
90 ggt cgt ggc tgt gca gag ccc aat cgc cca ggt gtc tat gcc aag gta      672
91 Gly Arg Gly Cys Ala Glu Pro Asn Arg Pro Gly Val Tyr Ala Lys Val
92           210             215             220
94 gca gag ttc ctg gac tgg atc cat gac act gtg cag gtc cgc tag         717
95 Ala Glu Phe Leu Asp Trp Ile His Asp Thr Val Gln Val Arg
96 225             230             235
99 <210> SEQ ID NO: 2
100 <211> LENGTH: 238
101 <212> TYPE: PRT
102 <213> ORGANISM: Mus sp.
104 <400> SEQUENCE: 2
106 Ile Val Gly Gly Gln Ala Val Ala Ser Gly Arg Trp Pro Trp Gln Ala
107 1               5               10              15
110 Ser Val Met Leu Gly Ser Arg His Thr Cys Gly Ala Ser Val Leu Ala
111           20              25              30
114 Pro His Trp Val Val Thr Ala Ala His Cys Met Tyr Ser Phe Arg Leu
115           35              40              45
118 Ser Arg Leu Ser Ser Trp Arg Val His Ala Gly Leu Val Ser His Gly
119     50              55              60
122 Ala Val Arg Gln His Gln Gly Thr Met Val Glu Lys Ile Ile Pro His
123 65              70              75              80
126 Pro Leu Tyr Ser Ala Gln Asn His Asp Tyr Asp Val Ala Leu Leu Gln
127           85              90              95
130 Leu Arg Thr Pro Ile Asn Phe Ser Asp Thr Val Asp Ala Val Cys Leu
131           100             105             110
134 Pro Ala Lys Glu Gln Tyr Phe Pro Trp Gly Ser Gln Cys Trp Val Ser
135           115             120             125
138 Gly Trp Gly His Thr Asp Pro Ser His Thr His Ser Ser Asp Thr Leu
139           130             135             140
```

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              RAW SEQUENCE LISTING              DATE: 02/26/2002
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              Input Set : A:\sequence listing.txt
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```

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142 Gln Asp Thr Met Val Pro Leu Leu Ser Thr His Leu Cys Asn Ser Ser
143 145             150             155             160
146 Cys Met Tyr Ser Gly Ala Leu Thr His Arg Met Leu Cys Ala Gly Tyr
147             165             170             175
150 Leu Asp Gly Arg Ala Asp Ala Cys Gln Gly Asp Ser Gly Gly Pro Leu
151             180             185             190
154 Val Cys Pro Ser Gly Asp Thr Trp His Leu Val Gly Val Val Ser Trp
155         195             200             205
158 Gly Arg Gly Cys Ala Glu Pro Asn Arg Pro Gly Val Tyr Ala Lys Val
159     210             215             220
162 Ala Glu Phe Leu Asp Trp Ile His Asp Thr Val Gln Val Arg
163 225             230             235
166 <210> SEQ ID NO: 3
167 <211> LENGTH: 1685
168 <212> TYPE: DNA
169 <213> ORGANISM: Mus sp.
171 <220> FEATURE:
172 <221> NAME/KEY: CDS
173 <222> LOCATION: (247)..(1065)
174 <223> OTHER INFORMATION:
177 <220> FEATURE:
178 <221> NAME/KEY: mat_peptide
179 <222> LOCATION: (352)..()
180 <223> OTHER INFORMATION:
183 <400> SEQUENCE: 3
184 ctcacatgta tctttcagaa taaatggaga ggatcttctg cttcaagtac aagtaagagc      60
186 tcggccagac tggctcctgg tatgccatga gggccggagc ccagccctgg gcatgcacat     120
188 ctgcaagagt cttgggcata tcaggcttac tcaacacaag gccgtgaatc tgtctgacat     180
190 caagctcaac agatcccagg agtttgctca actctctgct agaccgggag gccttgtaga     240
192 ggaggc atg gaa gcc cag gta ggg ctt ctg tgg gtt agc gct aac tgt       288
193        Met Glu Ala Gln Val Gly Leu Leu Trp Val Ser Ala Asn Cys
194         -35             -30             -25
196 cct tct ggc cga att gtt tct ctc aaa tgt tct gag tgt ggg gca agg     336
197 Pro Ser Gly Arg Ile Val Ser Leu Lys Cys Ser Glu Cys Gly Ala Arg
198     -20             -15             -10
200 cct ctg gct tct cga ata gtt ggc ggc caa gct gtg gct tct ggg cgc     384
201 Pro Leu Ala Ser Arg Ile Val Gly Gly Gln Ala Val Ala Ser Gly Arg
202 -5             -1  1             5             10
204 tgg cca tgg caa gct agc gtg atg ctt ggc tcc cgg cac acg tgt ggg     432
205 Trp Pro Trp Gln Ala Ser Val Met Leu Gly Ser Arg His Thr Cys Gly
206             15             20             25
208 gcc tct gtg ttg gca cca cac tgg gta gtg act gct gcc cac tgc atg     480
209 Ala Ser Val Leu Ala Pro His Trp Val Val Thr Ala Ala His Cys Met
210         30             35             40
212 tac agt ttc agg ctg tcc cgc cta tcc agc tgg cgg gtt cat gca ggg     528
213 Tyr Ser Phe Arg Leu Ser Arg Leu Ser Ser Trp Arg Val His Ala Gly
214     45             50             55
216 ctg gtc agc cat ggt gct gtc cga caa cac cag gga act atg gtg gag     576
217 Leu Val Ser His Gly Ala Val Arg Gln His Gln Gly Thr Met Val Glu
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PATENT APPLICATION:   US/09/856,371A    TIME: 09:28:41

Input Set : A:\sequence listing.txt
Output Set: N:\CRF3\02262002\I856371A.raw

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218 60                      65              70              75
220 aag atc att cct cat cct ttg tac agt gcc cag aac cat gac tat gat    624
221 Lys Ile Ile Pro His Pro Leu Tyr Ser Ala Gln Asn His Asp Tyr Asp
222            80                  85              90
224 gtg gct ctg ctg cag ctc cgg aca cca atc aac ttc tca gac acc gtg    672
225 Val Ala Leu Leu Gln Leu Arg Thr Pro Ile Asn Phe Ser Asp Thr Val
.226           95                 100              105
228 gac gct gtg tgc ttg ccg gcc aag gag cag tac ttt cca tgg ggg tcg    720
229 Asp Ala Val Cys Leu Pro Ala Lys Glu Gln Tyr Phe Pro Trp Gly Ser
230           110                 115              120
232 cag tgc tgg gtg tct ggc tgg ggc cac acc gac ccc agc cat act cat    768
233 Gln Cys Trp Val Ser Gly Trp Gly His Thr Asp Pro Ser His Thr His
234           125                 130              135
236 agc tca gat aca ctg cag gac aca atg gta ccc ctg ctc agc acc cac    816
237 Ser Ser Asp Thr Leu Gln Asp Thr Met Val Pro Leu Leu Ser Thr His
238 140                145              150              155
240 ctc tgc aac agc tca tgc atg tac agt ggg gca ctt aca cac cgc atg    864
241 Leu Cys Asn Ser Ser Cys Met Tyr Ser Gly Ala Leu Thr His Arg Met
242           160                 165              170
244 ttg tgt gct ggc tac ctg gat gga agg gca gac gca tgc cag gga gac    912
245 Leu Cys Ala Gly Tyr Leu Asp Gly Arg Ala Asp Ala Cys Gln Gly Asp
246           175                 180              185
248 agc ggg gga ccc ctg gta tgt ccc agt ggt gac acg tgg cac ctt gta    960
249 Ser Gly Gly Pro Leu Val Cys Pro Ser Gly Asp Thr Trp His Leu Val
250           190                 195              200
252 ggg gtg gtc agc tgg ggt cgt ggc tgt gca gag ccc aat cgc cca ggt    1008
253 Gly Val Val Ser Trp Gly Arg Gly Cys Ala Glu Pro Asn Arg Pro Gly
254           205                 210              215
256 gtc tat gcc aag gta gca gag ttc ctg gac tgg atc cat gac act gtg    1056
257 Val Tyr Ala Lys Val Ala Glu Phe Leu Asp Trp Ile His Asp Thr Val
258 220                225              230              235
260 cag gtc cgc tagccgaaga agcagcagca gccacctgtg acgccgagct            1105
261 Gln Val Arg
264 gtggatcgcc catggatcac cccagtctgg gggccagcat ctgggtcact gggcctctcc  1165
266 ccaaaggctc tgacttcgag ttcatctttc tcatctgaga acctccacaa caggaaaagg  1225
268 agtctgcggc tagattggga atgatggtga gaggaaggga taggaggaca gaagagacag  1285
270 cagaggcttc tggaagcatc tgggagactg ctcctctgct cccccacac cccacgtgca    1345
272 tccactgggg gatgctggag atgcccaatc cttgtttctt gtggggccac tggaaggcta  1405
274 agtccaactt tagaggatgc cctgtctcga gagttactag gcagataagg ttaaggttgg  1465
276 acaagctcag gtaaaggcac ggaagtcaag atccctctc ccccgtgcgg tcctgttctg    1525
278 aggtaagcta atagccccgc accaggcaga ggtctacagg gtaagaagga tgcagttggg  1585
280 ctacacgacg ctattttca aatgatgttt ctgtaaattg gttgagagag ttttgttatt    1645
282 aaacagaaat tatgtataaa aaaaaaaaa aaaaaaaaa                           1685
285 <210> SEQ ID NO: 4
286 <211> LENGTH: 273
287 <212> TYPE: PRT
288 <213> ORGANISM: Mus sp.
290 <400> SEQUENCE: 4
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RAW SEQUENCE LISTING            DATE: 02/26/2002
PATENT APPLICATION:  US/09/856,371A      TIME: 09:28:41

Input Set : A:\sequence listing.txt
Output Set: N:\CRF3\02262002\I856371A.raw

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293 -35                    -30                    -25                    -20
296 Gly Arg Ile Val Ser Leu Lys Cys Ser Glu Cys Gly Ala Arg Pro Leu
297                    -15                    -10                    -5
300 Ala Ser Arg Ile Val Gly Gly Gln Ala Val Ala Ser Gly Arg Trp Pro
301         -1  1               5                    10
304 Trp Gln Ala Ser Val Met Leu Gly Ser Arg His Thr Cys Gly Ala Ser
305     15                  20                    25
308 Val Leu Ala Pro His Trp Val Val Thr Ala Ala His Cys Met Tyr Ser
309 30                  35                    40                    45
312 Phe Arg Leu Ser Arg Leu Ser Ser Trp Arg Val His Ala Gly Leu Val
313             50                    55                    60
316 Ser His Gly Ala Val Arg Gln His Gln Gly Thr Met Val Glu Lys Ile
317             65                    70                    75
320 Ile Pro His Pro Leu Tyr Ser Ala Gln Asn His Asp Tyr Asp Val Ala
321         80                    85                    90
324 Leu Leu Gln Leu Arg Thr Pro Ile Asn Phe Ser Asp Thr Val Asp Ala
325     95                    100                   105
328 Val Cys Leu Pro Ala Lys Glu Gln Tyr Phe Pro Trp Gly Ser Gln Cys
329 110                   115                   120                   125
332 Trp Val Ser Gly Trp Gly His Thr Asp Pro Ser His Thr His Ser Ser
333             130                   135                   140
336 Asp Thr Leu Gln Asp Thr Met Val Pro Leu Leu Ser Thr His Leu Cys
337             145                   150                   155
340 Asn Ser Ser Cys Met Tyr Ser Gly Ala Leu Thr His Arg Met Leu Cys
341         160                   165                   170
344 Ala Gly Tyr Leu Asp Gly Arg Ala Asp Ala Cys Gln Gly Asp Ser Gly
345     175                   180                   185
348 Gly Pro Leu Val Cys Pro Ser Gly Asp Thr Trp His Leu Val Gly Val
349 190                   195                   200                   205
352 Val Ser Trp Gly Arg Gly Cys Ala Glu Pro Asn Arg Pro Gly Val Tyr
353             210                   215                   220
356 Ala Lys Val Ala Glu Phe Leu Asp Trp Ile His Asp Thr Val Gln Val
357         225                   230                   235
360 Arg
364 <210> SEQ ID NO: 5
365 <211> LENGTH: 2068
366 <212> TYPE: DNA
367 <213> ORGANISM: Mus sp.
369 <220> FEATURE:
370 <221> NAME/KEY: CDS
371 <222> LOCATION: (516)..(1448)
372 <223> OTHER INFORMATION:
375 <220> FEATURE:
376 <221> NAME/KEY: mat_peptide
377 <222> LOCATION: (735)..()
378 <223> OTHER INFORMATION:
381 <400> SEQUENCE: 5
382 ctggctgggc tgttgaatca atcccgacat gaggacagga gcctcaccct gcccagcaga      60
384 acttactgcc ttatatcagt gcagctgact catatgagtc caacactgga tgaccaaagc     120
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Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY                    DATE: 02/26/2002
PATENT APPLICATION:   US/09/856,371A       TIME: 09:28:42

      Input Set : A:\sequence listing.txt
      Output Set: N:\CRF3\02262002\I856371A.raw

L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:1359 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20
L:1389 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21